REPLACEMENT SHEET

FIGURE 4

A.

SEQ ID NO:63 - AME 5 light chain variable region amino acid sequence

DIQMTQSPSSLSASVGDRVTITCRASSSVHYIHWYQQKPGKVPKLLIYATSGLAS
GVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQTWTFNPPTFGGGTKVEIK

B.

SEQ ID NO:64 - AME 5 light chain variable region nucleic acid sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGA
GACAGAGTCACCATCACTTGCAGGGCCAGCTCAAGTGTACATTACATC
CACTGGTACCAGCAGAAACCAGGGAAAGTTCCTAAGCTCTTGATCTAT
GCCACATCCGGCCTGGCTTCTGGGGTCCCATCTCGGTTCAGTGGCAGT
GGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAA
GATGTTGCCACTTATTACTGCCAGACTTGGACTTTTAACCCTCCCACG
TTCGGCGGAGGGACCAAGGTGGAGATCAAA

FIGURE 5

A.

SEQ ID NO:65 - AME 5 heavy chain variable region amino acid sequence

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNMHWVRQAPGQGLEWMGAIY
PGNGDTSYNQKFKWRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSTYYGGD
WQFDEWGKGTTVTVSS

B.

SEQ ID NO:66 - AME 5 heavy chain variable region nucleic acid sequence

CAGGTGCAGCTGGTGCAGTCTGGTGCTGAAGTGAAGAAGCCTGGGGCC
TCAGTGAAGGTGTCCTGCAAGGCATCTGGATACACCTTCACCAGCTAC
AATATGCACTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGAGCCATCTATCCTGGAAATGGTGATACAAGCTACAATCAGAAGTTT
AAATGGAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTAC
ATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT
GCGAGATCGACTTATTACGGCGGTGACTGGCAGTTCGACGAGTGGGGC
AAAGGGACCACGGTCACCGTCTCCTCA

ANNOTATED SHEET- Deleted Figure 8

FIGURE 8

A. Amino acid sequence of a human light chain framework region Vkl (DPK4) (A20) with interspersed CDR sequences labeled

(FRL1 - SEQ ID NO:87) (CDRL1) (FRL2 - SEQ ID NO:88) (CDRL2)
DIQMTQSPSSLSASVGDRVTITCXXXXXXXXXXWYQQKPGKVPKLLIYXXXXXXX

(FRL3 - SEQ ID NO:89) (CDRL3) (FRL4 - SEQ ID NO:90)
GVPSRFSGSGSGTDFTLTISSLQPEDVATYYCXXXXXXXXXFGGGTKVEIK

B. Nucleic acid sequence of a human light chain framework region Vkl (DPK4) (A20) with interspersed CDR sequences labeled

(FRL1 - SEQ ID NO:91)
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAG

(CDRL1)
TCACCATCACTTGCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTGGTACCAG

(FRL2 - SEQ ID NO:92) (CDRL2)
CAGAAACCAGGGAAAGTTCCTAAGCTCTTGATCTATXXXXXXXXXXXXXXXXX

(CDRL2 cont.) (FRL3 - SEQ ID NO:93)
XXXXGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCT

CACCATCAGCAGCCTGCAGCCTGAAGATGTTGCCACTTATTACTGCXXXXXXXXX

(CDRL3) (FRL4 - SEQ ID NO:94)
XXXXXXXXXXXXXXXXXXXTTCGGCGGAGGGACCAAGGTGGAGA

TCAAA

ANNOTATED SHEET- Deleted Figure 9

~~FIGURE 9~~

~~A. Amino acid sequence of a human heavy chain framework region VHI DP7/21-2 with interspersed CDR sequences labeled~~

~~(FRH1 – SEQ ID NO:95) (CDRH1) (FRH2 – SEQ ID NO:96)~~
~~QVQLVQSGAEVKKPGASVKVSCKAS~~XXXXXXXXXX~~WVRQAPGQGLEWMG~~

~~(CDRH2) (FRH3 – SEQ ID NO:97)~~
~~XXXXXXXXXXXXXXXXX~~RVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR

~~(CDRH3) (FRH4 – SEQ ID NO:98)~~
~~XXXXXXXXXXX~~WGKGTTVTVSS

~~B. Nucleic acid sequence of a human heavy chain framework region VHI DP7/21-2 with interspersed CDR sequences labeled~~

~~(FRH1 – SEQ ID NO:99)~~
~~CAGGTGCAGCTGGTGCAGTCTGGTGCTGAAGTGAAGAAGCCTGGGGCCTCAGTG~~

~~(CDRH1)~~
~~AAGGTGTCCTGCAAGGCATCT~~XXXXXXXXXXXXXXXXXXXXXXXXXXXXXX~~TG~~

~~(FRH2 – SEQ ID NO:100) (CDRH2)~~
~~GGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGA~~XXXXXXXXXXXXX

~~(CDRH2 cont.)~~
~~XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX~~AGAGTCACCATGAC

~~(FRH3 – SEQ ID NO:101)~~
~~CAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGA~~

~~(CDRH3)~~
~~GGACACGGCCGTGTATTACTGTGCGAGA~~XXXXXXXXXXXXXXXXXXXXXXXXX

~~(CDRH3) (FRH4 – SEQ ID NO:102)~~
~~XXXXXXXXXXX~~TGGGGCAAAGGGACCACGGTCACCGTCTCCTCA

FIGURE 6

A.

SEQ ID NO:67 - AME 33 complete light chain amino acid sequence

EIVLTQSPGTLSLSPGERATLSCRASSSVPYIHWYQQKPGQAPRLLIYATSALASGIPDR
FSGSGSGTDFTLTISRLEPEDFAVYYCQQWLSNPPTFGQGTKLEIKRTVAAPSVFIFPPS
DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

- Constant Region is underlined

B.

SEQ ID NO:68 - AME 33 complete light chain nucleic acid sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAG
CCACCCTCTCCTGCAGGGCCAGCTCAAGTGTACCGTACATCCACTGGTACCAGCA
GAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGCCACATCCGCTCTGGCTTCTG
GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCAT
CAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTGGCTGAGT
AACCCACCCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTG
CACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCC
TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA
AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA
CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGA
CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG
CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

REPLACEMENT SHEET

FIGURE 7

A. SEQ ID NO:69 - AME 33 complete heavy chain amino acid sequence

EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYPLTG
DTSYNQKSKLQVTISADKSISTAYLQWSSLKASDTAMYYCARSTYVGGDWQFDVWG
KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

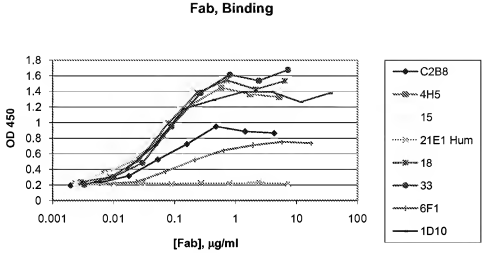
- Constant Region is underlined; the "D" at position 280 and "K" at position 290 are in bold

B. SEQ ID NO:70 - AME 33 complete heavy chain nucleic acid sequence

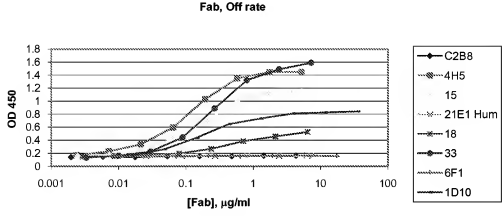
GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTG
AAGATCTCCTGTAAGGGTTCTGGCCGTACATTTACCAGTTACAATATGCACTGGGT
GCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGGCTATTTATCCCTTGACG
GGTGATACTTCCTACAATCAGAAGTCGAAACTCCAGGTCACCATCTCAGCCGACA
AGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGC
CATGTATTACTGTGCGAGATCGACTTACGTGGGCGGTGACTGGCAGTTCGATGTCT
GGGGCAAGGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT
CTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACT
CCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTTGAGCC
CAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG
GGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTC
CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTG**GAC**GGCGTGGAGGTGCATAATGCCAAGACAAAG
CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC
TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGA
ACCACAGGTGTACACCCTGCCCCCATCCCGGGACGAGCTGACCAAGAACCAGGTC
AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC
CGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACA
CGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

FIGURE 8

A.


Fab, Binding
OD 450
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
100
[Fab], µg/ml
C2B8
4H5
15
21E1 Hum
18
33
6F1
1D10

B.


Fab, Off rate
OD 450
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
100
[Fab], µg/ml
C2B8
4H5
15
21E1 Hum
18
33
6F1
1D10

C.

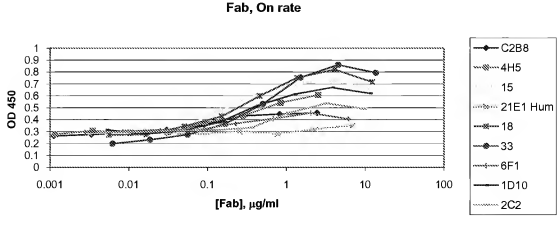
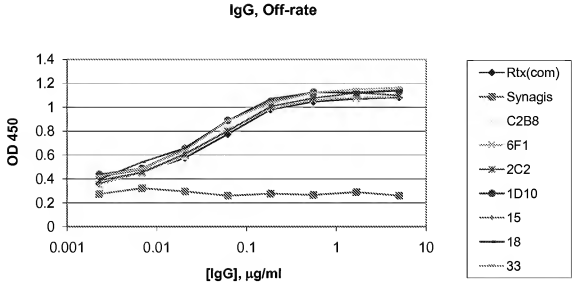

Fab, On rate
OD 450
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0.001
0.01
0.1
1
10
100
[Fab], µg/ml
C2B8
4H5
15
21E1 Hum
18
33
6F1
1D10
2C2

FIGURE 9

A.


IgG, Off-rate
OD 450
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
[IgG], µg/ml
Rtx(com)
Synagis
C2B8
6F1
2C2
1D10
15
18
33

B.

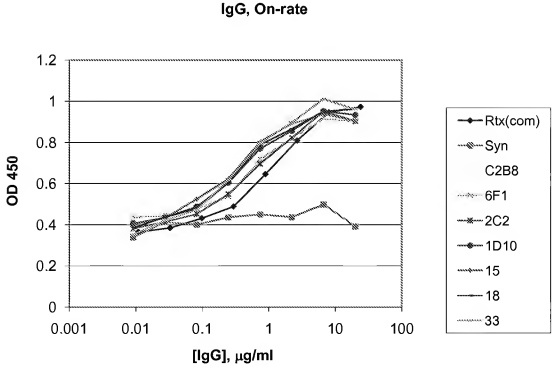
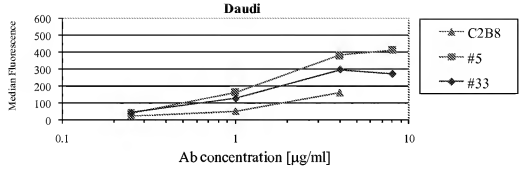
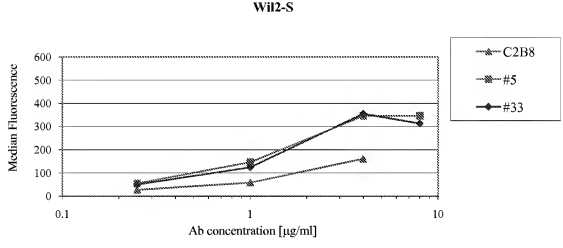

IgG, On-rate
OD 450
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
100
[IgG], µg/ml
Rtx(com)
Syn
C2B8
6F1
2C2
1D10
15
18
33

FIGURE 10

A.



B.



C.

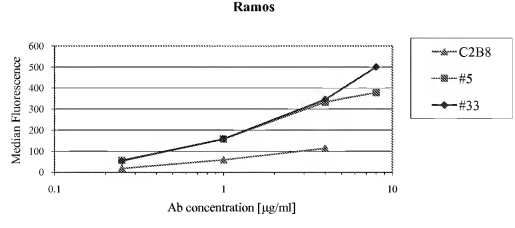


FIGURE 11

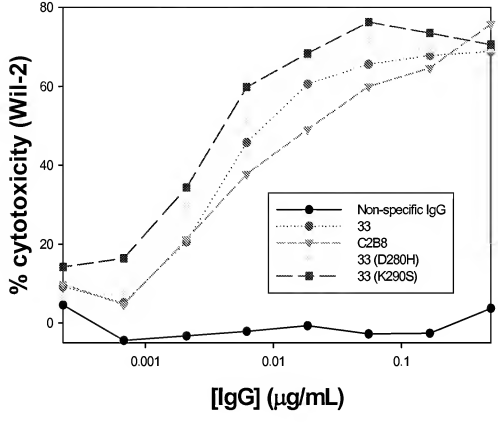

% cytotoxicity (Wil-2)
80
60
40
20
0
0.001
0.01
0.1
[IgG] (μg/mL)
Non-specific IgG
33
C2B8
33 (D280H)
33 (K290S)

FIGURE 12

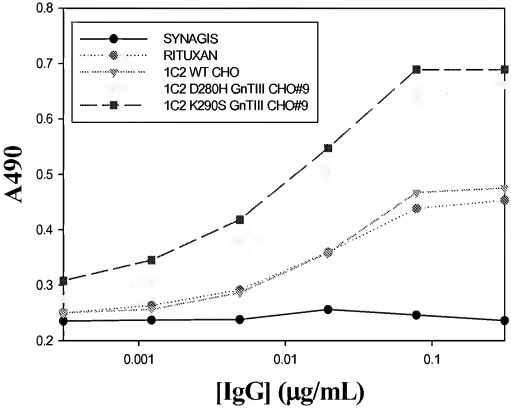
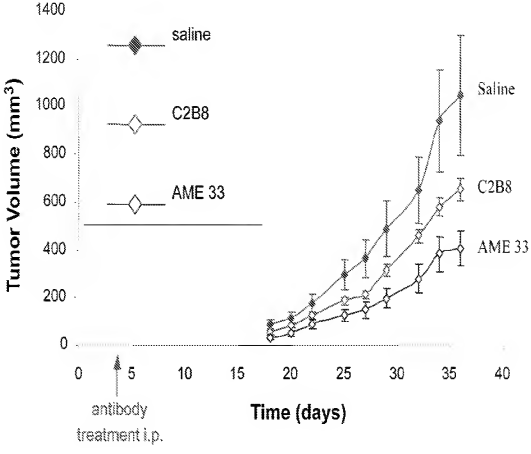

SYNAGIS
RITUXAN
1C2 WT CHO
1C2 D280H GnTIII CHO#9
1C2 K290S GnTIII CHO#9
A490
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.001
0.01
0.1
[IgG] (µg/mL)

FIGURE 13


1400
1200
1000
800
600
400
200
0
Tumor Volume (mm3)
saline
C2B8
AME 33
Saline
C2B8
AME 33
0
5
10
15
20
25
30
35
40
antibody
treatment i.p.
Time (days)